

OIKE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/811,285

DATE: 04/09/2001

TIME: 09:36:45

Input Set : A:\ADRB2_US2.app

Output Set: N:\CRF3\04092001\I811285.raw

ENTERED

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3 <110> APPLICANT: Drysdale, Connie M
4     Judson, Richard S
5     Liggett, Stephen B
6     Nandabalan, Krishnan
7     Stephens, J. Claiborne
11 <120> TITLE OF INVENTION: Association of beta2-adrenergic receptor haplotypes
12     with drug response
14 <130> FILE REFERENCE: MWH-0303US2
C--> 16 <140> CURRENT APPLICATION NUMBER: US/09/811,285
C--> 17 <141> CURRENT FILING DATE: 2001-03-16
19 <160> NUMBER OF SEQ ID NOS: 18
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 3451
25 <212> TYPE: DNA
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29 <221> NAME/KEY: CDS
30 <222> LOCATION: (1588)..(2829)
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37 aggatctttt gctttctata gcttcaaaat gttcttaatg ttaagacatt cttataactc 180
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49 tccaaagggt aaaactgtct tcatgcctgc aaattcctaa ggagggcacc taaagtactt 540
51 gacagcgagt gtgctgagga aatcggcagc tgttgaagtc acctcctgtg ctcttgccaa 600
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86          Met Gly Gln Pro Gly Asn Gly Ser Ala
87          1          5
89 ttc ttg ctg gca ccc aat aga agc cat gcg ccg gac cac gac gtc acg 1662
90 Phe Leu Leu Ala Pro Asn Arg Ser His Ala Pro Asp His Asp Val Thr
91 10          15          20          25
93 cag caa agg gac gag gtg tgg gtg ggc atg ggc atc gtc atg tct 1710
94 Gln Gln Arg Asp Glu Val Trp Val Val Gly Met Gly Ile Val Met Ser
95          30          35          40
97 ctc atc gtc ctg gcc atc gtg ttt ggc aat gtg ctg gtc atc aca gcc 1758
98 Leu Ile Val Leu Ala Ile Val Phe Gly Asn Val Leu Val Ile Thr Ala
99          45          50          55
101 att gcc aag ttc gag cgt ctg cag acg gtc acc aac tac ttc atc act 1806
102 Ile Ala Lys Phe Glu Arg Leu Gln Thr Val Thr Asn Tyr Phe Ile Thr
103          60          65          70
105 tca ctg gcc tgt gct gat ctg gtc atg ggc ctg gca gtg gtg ccc ttt 1854
106 Ser Leu Ala Cys Ala Asp Leu Val Met Gly Leu Ala Val Val Pro Phe
107          75          80          85
109 ggg gcc gcc cat att ctt atg aaa atg tgg act ttt ggc aac ttc tgg 1902
110 Gly Ala Ala His Ile Leu Met Lys Met Trp Thr Phe Gly Asn Phe Trp
111 90          95          100          105
113 tgc gag ttt tgg act tcc att gat gtg ctg tgc gtc acg gcc agc att 1950
114 Cys Glu Phe Trp Thr Ser Ile Asp Val Leu Cys Val Thr Ala Ser Ile
115          110          115          120
117 gag acc ctg tgc gtg atc gca gtg gat cgc tac ttt gcc att act tca 1998
118 Glu Thr Leu Cys Val Ile Ala Val Asp Arg Tyr Phe Ala Ile Thr Ser
119          125          130          135
121 cct ttc aag tac cag agc ctg ctg acc aag aat aag gcc cgg gtg atc 2046
122 Pro Phe Lys Tyr Gln Ser Leu Leu Thr Lys Asn Lys Ala Arg Val Ile
123          140          145          150
125 att ctg atg gtg tgg att gtg tca ggc ctt acc tcc ttc ttg ccc att 2094
126 Ile Leu Met Val Trp Ile Val Ser Gly Leu Thr Ser Phe Leu Pro Ile
127          155          160          165
129 cag atg cac tgg tac cgg gcc acc cac cag gaa gcc atc aac tgc tat 2142
130 Gln Met His Trp Tyr Arg Ala Thr His Gln Glu Ala Ile Asn Cys Tyr
131 170          175          180          185
133 gcc aat gag acc tgc tgt gac ttc ttc acg aac caa gcc tat gcc att 2190
134 Ala Asn Glu Thr Cys Asp Phe Phe Thr Asn Gln Ala Tyr Ala Ile
135          190          195          200
137 gcc tct tcc atc gtg tcc ttc tac gtt ccc ctg gtg atc atg gtc ttc 2238
138 Ala Ser Ser Ile Val Ser Phe Tyr Val Pro Leu Val Ile Met Val Phe
139          205          210          215
141 gtc tac tcc agg gtc ttt cag gag gcc aaa agg cag ctc cag aag att 2286
142 Val Tyr Ser Arg Val Phe Gln Glu Ala Lys Arg Gln Leu Gln Lys Ile
143          220          225          230
145 gac aaa tct gag ggc cgc ttc cat gtc cag aac ctt agc cag gtg gag 2334
146 Asp Lys Ser Glu Gly Arg Phe His Val Gln Asn Leu Ser Gln Val Glu
147          235          240          245
149 cag gat ggg cgg acg ggg cat gga ctc cgc aga tct tcc aag ttc tgc 2382
150 Gln Asp Gly Arg Thr Gly His Gly Leu Arg Arg Ser Ser Lys Phe Cys

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151 250          255          260          265
153 ttg aag gag cac aaa gcc ctc aag acg tta ggc atc atc atg ggc act 2430
154 Leu Lys Glu His Lys Ala Leu Lys Thr Leu Gly Ile Ile Met Gly Thr
155          270          275          280
157 ttc acc ctc tgc tgg ctg ccc ttc ttc atc gtt aac att gtg cat gtg 2478
158 Phe Thr Leu Cys Trp Leu Pro Phe Phe Ile Val Asn Ile Val His Val
159          285          290          295
161 atc cag gat aac ctc atc cgt aag gaa gtt tac atc ctc cta aat tgg 2526
162 Ile Gln Asp Asn Leu Ile Arg Lys Glu Val Tyr Ile Leu Leu Asn Trp
163          300          305          310
165 ata ggc tat gtc aat tct ggt ttc aat ccc ctt atc tac tgc cgg agc 2574
166 Ile Gly Tyr Val Asn Ser Gly Phe Asn Pro Leu Ile Tyr Cys Arg Ser
167          315          320          325
169 cca gat ttc agg att gcc ttc cag gag ctt ctg tgc ctg cgc agg tct 2622
170 Pro Asp Phe Arg Ile Ala Phe Gln Glu Leu Leu Cys Leu Arg Arg Ser
171 330          335          340          345
173 tct ttg aag gcc tat ggg aat ggc tac tcc agc aac ggc aac aca ggg 2670
174 Ser Leu Lys Ala Tyr Gly Asn Gly Tyr Ser Ser Asn Gly Asn Thr Gly
175          350          355          360
177 gag cag agt gga tat cac gtg gaa cag gag aaa gaa aat aaa ctg ctg 2718
178 Glu Gln Ser Gly Tyr His Val Glu Gln Glu Lys Glu Asn Lys Leu Leu
179          365          370          375
181 tgt gaa gac ctc cca ggc acg gaa gac ttt gtg ggc cat caa ggt act 2766
182 Cys Glu Asp Leu Pro Gly Thr Glu Asp Phe Val Gly His Gln Gly Thr
183          380          385          390
185 gtg cct agc gat aac att gat tca caa ggg agg aat tgt agt aca aat 2814
186 Val Pro Ser Asp Asn Ile Asp Ser Gln Gly Arg Asn Cys Ser Thr Asn
187          395          400          405
189 gac tca ctg ctg taa1 agcagttttt ctacttttaa agaccccccc ccccccaaca 2869
190 Asp Ser Leu Leu
191 410
193 gaacactaaa cagactatatt aacttgaggg taataaaactt agaataaaat tgtaaaaatt 2929
195 gtatagagat atgcagaagg aagggcatcc ttctgccttt tttatTTTTT taagctgtaa 2989
197 aaagagagaa aacttatttg agtgattatt tggtatttgt acagttcagt tcctctttgc 3049
199 atggaatttg taagtattatg tctaaagagc tttagtctta gaggacctga gtctgtctata 3109
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207 cacggggtat tttaggcagg gatttgagga gcagcttcag ttgttttccc gagcaaaggt 3349
209 ctaaagttta cagtaaataa aatgtttgac catgccttca ttgcacctgt ttgtccaaaa 3409
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223          20          25          30
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226 Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu
227          50          55          60
228 Gln Thr Val Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu
229          65          70          75          80
230 Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ala His Ile Leu Met
231          85          90          95
232 Lys Met Trp Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile
233          100         105         110
234 Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala
235          115         120         125
236 Val Asp Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Tyr Gln Ser Leu
237          130         135         140
238 Leu Thr Lys Asn Lys Ala Arg Val Ile Ile Leu Met Val Trp Ile Val
239          145         150         155         160
240 Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His Trp Tyr Arg Ala
241          165         170         175
242 Thr His Gln Glu Ala Ile Asn Cys Tyr Ala Asn Glu Thr Cys Cys Asp
243          180         185         190
244 Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser Ile Val Ser Phe
245          195         200         205
246 Tyr Val Pro Leu Val Ile Met Val Phe Val Tyr Ser Arg Val Phe Gln
247          210         215         220
248 Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser Glu Gly Arg Phe
249          225         230         235         240
250 His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly Arg Thr Gly His
251          245         250         255
252 Gly Leu Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu His Lys Ala Leu
253          260         265         270
254 Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu Cys Trp Leu Pro
255          275         280         285
256 Phe Phe Ile Val Asn Ile Val His Val Ile Gln Asp Asn Leu Ile Arg
257          290         295         300
258 Lys Glu Val Tyr Ile Leu Asn Trp Ile Gly Tyr Val Asn Ser Gly
259          305         310         315         320
260 Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe Arg Ile Ala Phe
261          325         330         335
262 Gln Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys Ala Tyr Gly Asn
263          340         345         350
264 Gly Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser Gly Tyr His Val
265          355         360         365
266 Glu Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp Leu Pro Gly Thr
267          370         375         380
268 Glu Asp Phe Val Gly His Gln Gly Thr Val Pro Ser Asp Asn Ile Asp
269          385         390         395         400
270 Ser Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu Leu
271          405         410

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286 <212> TYPE: DNA
287 <213> ORGANISM: Homo sapiens
289 <400> SEQUENCE: 4
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293 <210> SEQ ID NO: 5
294 <211> LENGTH: 15
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/811,285

DATE: 04/09/2001

TIME: 09:36:46

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L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date